SEQUENCE LISTING

<110> ASAKURA, YOKO
 NAKAMURA, JUN
 KANNO, SOHEI
 SUGA, MIKIKO
 KIMURA, EIICHIRO
 ITO, HISAO
 MATSUI, KAZUHIKO
 OHSUMI, TSUYOSHI
 NAKAMATSU, TSUYOSHI
 KURAHASHI, OSAMU

RECEIVED

NOV 2 6 2003

TECH CENTER 1600/2900

<120> METHOD OF CONSTRUCTING AMINO ACID PRODUCING BACTERIAL STRAINS, AND METHOD OF PREPARING AMINO ACIDS BY FERMENTATION WITH THE CONSTRUCTED AMINO ACID PRODUCING BACTERIAL STRAINS

4 1

<130> 0010-1108-0 CONT <140> 09/577,005 <141> 2000-05-25 <150> PCT/JP99/05175 <151> 1999-09-22 <150> JP 271786/1998 <151> 1998-09-25 <150> JP 271787/1998 1998-09-25 <151> <160> 66 <170> PatentIn version 3.1 <210> 1 <211> 46 <212> DNA <213> Artificial sequence

ttaattottt gtggtoatat otgogacact gooataattt gaacgt
<210> 2
<211> 46

46

<210> 2 <211> 46 <212> DNA <213> Artificial sequence <220> <223> Synthetic DNA

<223> Synthetic DNA

<220>

<400> 1

<400> ttaatto	tettt geggteatat etgegaeact geeataattt gaaegt	46
<210> <211> <212> <213>	46 DNA	•
<220> <223>		
<400> ttaatto	3 tcttt gtggtcatat ctgcgacact gctataattt gaacgt	46
<210> <211> <212> <213>	46 DNA	
<220> <223>		
<400> ttaatto	4 tettt gttgacatat etgegacaet getataattt gaaegt	. 46
<210> <211> <212> <213>	46 DNA	
<220> <223>		
<400> ttaatt	5 tcttt gttgccatat ctgcgacact gctataattt gaacgt	46
<210><211><211><212><213>	46 DNA	
<220> <223>		
<400> ttaatt	6 tcttt gttgtcatat ctgcgacact gctataattt gaacgt	46
	-2-	

<210> <211> <212> <213>	7 30 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400> gtcgac	7 aata gcctgaatct gttctggtcg	30
<210><211><211><212><213>	8 30 DNA Artificial sequence	
<22.0> <223>	Synthetic DNA	
<400> aagctt	8 atcg acgctcccct ccccaccgtt	30
<210> <211> <212> <213>	9 20 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400> atcggt	9 ataa cgtgttaacc	20
<210> <211> <212> <213>	10 20 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400> atcggt	10 ataa tgtgttaacc	. 20
<210><211><211><212><213>	11 40 DNA Artificial sequence	

<220: <223:		
<400	> 11	
	Egacaa aaccgcattt atcggtataa tgtgttaacc	4.0
		40
<210>		•
<211><212>		
<21,3>		
<220>		•
<223>	Synthetic DNA	
<400>	12	•
aggga	teegt ceagteteag acageate '	28
<210> <211>		٠,
<212>	DNA	
<213>	Artificial sequence	
<220>		
<223>	Synthetic DNA	
	•	
<400>	13	
	13 Bacag ctatgac	17
caggaa	aacag ctatgac	17
<210><211>	14 20	17
caggaa	14 20 DNA	17
<210><211><212><213>	14 20	17
<210><211><212><213> 220	14 20 DNA Artificial sequence	17
<210><211><212><213><223>	14 20 DNA Artificial sequence Synthetic DNA	17
<210><211><212><213><223><400>	14 20 DNA Artificial sequence	
<210><211><212><213><223><400>	14 20 DNA Artificial sequence Synthetic DNA	17
<210><211><212><213><223><400> <gaattc<<210></gaattc<<210>	14 20 DNA Artificial sequence Synthetic DNA 14 gctc ccggtgcagc	
<210><211><212><213><223><400> <gaatte< td=""><td>14 20 DNA Artificial sequence Synthetic DNA 14 gctc ccggtgcagc</td><td></td></gaatte<>	14 20 DNA Artificial sequence Synthetic DNA 14 gctc ccggtgcagc	
<210><211><212><213> 223 223 400 210 211	14 20 DNA Artificial sequence Synthetic DNA 14 getc ccggtgcage	
<pre><210> <211> <212> <213> <223> <400> gaattc <210> <211> <212> <213></pre>	14 20 DNA Artificial sequence Synthetic DNA 14 gctc ccggtgcagc 15 20 DNA Artificial sequence	
<210><211><212><213> 223 223 400 211 212 211 212 213	14 20 DNA Artificial sequence Synthetic DNA 14 gctc ccggtgcagc	
<pre><210> <211> <212> <213> <223> <400> gaattc <210> <211> <212> <213></pre>	14 20 DNA Artificial sequence Synthetic DNA 14 gctc ccggtgcagc 15 20 DNA Artificial sequence	

galgeagaat teettgtegg	
	20
<210> 16	
<210> 16 <211> 28	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic DNA	
<400> 16	
tggattgctg gctataatgg tgtcgtga	20
	28
<210> 17	
<211> 53	
<212> DNA	
<213> Artificial sequence	
sequence	
<220>	Ŷ.
<223> Synthetic DNA	
<400> 17	
caacccacgt tcagttgaca actactggat tootgant	
caacccacgt tcagttgaca actactggat tgctggctat aatggtgtcg tga	53
<210> 18	
<211> 53	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic DNA	
<400> 18	
caacccacgt tcagttgact actactggat tgctggctaa agtggtgtcg tga	
in the state of th	, 53
<210> 19	
<211> 28	
<212> DNA	
<213> Artificial sequence	
rectal sequence	,
<220>	
<223> Synthetic DNA	Ī
<223> Synthetic DNA <400> 19	Ī
<223> Synthetic DNA <400> 19	- I
<223> Synthetic DNA	28
<223> Synthetic DNA <400> 19 ggctgaaact gctataatag gcgccagc	28
<223> Synthetic DNA <400> 19	28

<211>	51
<212>	DNA
<213>	Artificial sequence
<220> <223>	Synthetic DNA
<400>	20 [°]
ggaaac	acgg cgttgccatg cggggctgaa actgctataa taggcgccag c 51
<210>	21
<211>	51
<212>	DNA
<213>	Artificial sequence
<220> <223>	Synthetic DNA
<400>	21
ggaaac	acgg cgttgacatg cggggctgaa actgctataa taggcgccag c 51
<210>	22
<211>	22
<212>	DNA
<213>	Artificial sequence
<220> <223>	Synthetic DNA
<400>	22
gtgcgg	gtcc agatgatctt ag 22
<210>	23
<211>	20
<212>	DNA
<213>	Artificial sequence
<220> <223>	Synthetic DNA
<400>	23
gggatc	ccgg atgaatgtca 20
<210><211><211><212><212><213>	24 23 DNA Artificial sequence
12107	-6-

```
<220>
<223> Synthetic DNA
<400> 24
                                                                           23
gcccggggtg ggcgaagaac tcc
<210> 25
<211> 23
<212> DNA
<213> Artificial sequence
<220>
<223> Synthetic DNA
<220>
<221> misc_feature
<222> (3)..(3)
<223> n = inosine
<220>
<221> misc_feature
<222> (6)..(6)
\langle 223 \rangle n = inosine
<220>
<221> misc_feature
<222> (9)..(9)
\langle 223 \rangle n = inosine
<220>
<221> misc_feature
<222> (15)..(15)
\langle 223 \rangle n = inosine
<220>
<221> misc feature
<222> (18)...(18)
\langle 223 \rangle n = inosine
<220>
<221> misc feature
<222> (21)..(21)
\langle 223 \rangle n = inosine
<400> 25
```

```
<210> 26
<211> 23
<212> DNA
<213> Artificial sequence
<220>
<223> Synthetic DNA
<220>
<221> misc feature
<222> (6)..(6)
\langle 223 \rangle n = inosine
<220>
<221> misc feature
<222> (12)..(12)
\langle 223 \rangle n = inosine
<220>
<221> misc feature
<222> (15)..(15)
\langle 223 \rangle n = inosine
<220>
<221> misc feature
<222> (18)..(18)
\langle 223 \rangle n = inosine
<220>
<221> misc feature
<222> (21)..(21)
\langle 223 \rangle n = inosine
<400> 26
ccttcnccgt tnagngtngt ncg
<210> 27
<211> 30
<212> DNA
<213> Artificial sequence
<220>
<223> Synthetic DNA
```

u .	· Pa	•			
<400> 27					
ttgcagttaa ccacgaaggt caggttgtcc					30
<210x 00					5 5
<210> 28 <211> 30					
<212> DNA				•	
<213> Artificial sequence					
<220>			•		
<223> Synthetic DNA					
<400> 28	•				
tggatgagac cacgtgattc tggctcgtcc					30
<210> 29					
<211> 30	. ,				
<212> DNA					
<213> Artificial sequence		•			
<220>					
<223> Synthetic DNA					•
<400> 29					
acagateetg caegaaggea teaaegagge					
- 55					30
<210> 30		•			
<211> 30					•
(212> DNA (213> Artificial sequence	•		•		
(213> Artificial sequence					
(220)					
223> Synthetic DNA					
400> 30					
categetge gggtacetee taegeeacee					
				•	30
210> 31					
211> 2766 212> DNA					
213> Brevibacterium lactofermentum <i>F</i>	maar s				
	ATCC13869				
220> 221> CDS					
222> (1)(2766)					
00> 31					
g gcc gat caa gca aaa ctt ggt ggt aa	a ccc +~~				
	y cee leg g	gat gac	tct aac		48
- <u>-</u> -9	9-				
					•
				*	

Met Ala Asp Gln Ala Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn 5 10 15	
ttc gcg atg atc cgc gat ggc gtg gca tct tat ttg aac gac tca gat Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp 20 25 30	96
ccg gag gag acc aac gag tgg atg gat tca ctc gac gga tta ctc cag Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln 35 40 45	144
gag tct tct cca gaa cgt gct cgt tac ctc atg ctt cgt ttg ctt gag Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu 50 55	192
cgt gca tct gca aag cgc gta tct ctt ccc cca atg acg tca acc gac Arg Ala Ser Ala Lys Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp 70 75 80	240
tac gtc aac acc att cca acc tct atg gaa cct gaa ttc cca ggc gat Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp 85 90 95	288
gag gaa atg gag aag cgt tac cgt cgt tgg att cgc tgg aac gcc Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala 100 105	336
atc atg gtt cac cgc gct cag cga cca ggc atc ggc gtc ggc gga cac Ile Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His 115 120 125	384
att tcc act tac gca ggc gca gcc cct ctg tac gaa gtt ggc ttc aac Ile Ser Thr Tyr Ala Gly Ala Ala Pro Leu Tyr Glu Val Gly Phe Asn 130 135	432
cac ttc ttc cgc ggc aag gat cac cca ggc ggc ggc gac cag atc ttc His Phe Phe Arg Gly Lys Asp His Pro Gly Gly Gly Asp Gln Ile Phe 155	480
ttc cag ggc cac gca tca cca ggt atg tac gca cgt gca ttc atg gag Phe Gln Gly His Ala Ser Pro Gly Met Tyr Ala Arg Ala Phe Met Glu 165 170	528
ggt cgc ctt tct gaa gac gat ctc gat ggc ttc cgt cag gaa gtt tcc Gly Arg Leu Ser Glu Asp Asp Leu Asp Gly Phe Arg Gln Glu Val Ser 180 185	576
cgt gag cag ggt ggc att ccg tcc tac cct cac cca cac ggt atg aag Arg Glu Gln Gly Gly Ile Pro Ser Tyr Pro His Pro His Gly Met Lys 200 205	624
gac ttc tgg gag ttc cca act gtg tcc atg ggt ctt ggc cca atg gat	672

Asp	Phe 210	_	Glu	Phe	Pro	Thr 215	Val	Ser	Met	Gly	Leu 220	Gly	Pro	Met	Asp	
								cgc Arg								720
								tgg Trp								768
								ctc Leu 265								816
								gtt Val								864
gac Asp	gga Gly 290	cct Pro	gtc Val	cgc Arg	ggt Gly	aac Asn 295	acc Thr	aag Lys	atc Ile	atc Ile	cag Gln 300	gaa Glu	ctc Leu	gag Glu	tcc Ser	912
ttc Phe 305	ttc Phe	cgt Arg	ggc Gly	gca Ala	ggc Gly 310	tgg Trp	tct Ser	gtg Val	atc Ile	aag Lys 315	gtt Val	gtt Val	tgg Trp	ggt Gly	cgc Arg 320	960
								gac Asp								1008
atc Ile	atg Met	aac Asn	aac Asn 340	acc Thr	tcc Ser	gat Asp	ggt Gly	gac Asp 345	tac Tyr	cag Gln	acc Thr	ttc Phe	aag Lys 350	gct Ala	aac Asn	1056
gac Asp	Gly	Ala	Tyr	Val	Arg	Glu	His	ttc Phe	Phe	Gly	Arg	Asp	Pro	cgc Arg	acc Thr	1104
								gac Asp								1152
cgt Arg 385	ggc Gly	ggc Gly	cac His	gat Asp	tac Tyr 390	cgc Arg	aag Lys	gtt Val	tac Tyr	gca Ala 395	gcc Ala	tac Tyr	aag Lys	cga Arg	gct Ala 400	1200
								gtc Val								1248
ggc	tac	gga	ctc	ggc	cac	aac	ttc	gaa	ggc	cgt	aac	gca	acc	cac	cag	1296

Gly	Tyr	Gly	Leu 420	Gly	His	Asn	Phe	Glu 425	Gly	Arg	Asn	Ala	Thr 430	His	Gln		
	aag Lys																1344
	atc Ile 450														cct Pro		1392
	tac Tyr																1440
	cgt Arg																1488
tac Tyr	gat Asp	cca Pro	att Ile 500	cag Gln	gtt Val	cca Pro	cca Pro	ctg Leu 505	gat Asp	aag Lys	ctt Leu	cgc Arg	tct Ser 510	gtc Val	cgt Arg		1536
	ggc Gly																1584
	ttc Phe 530																1632
	atc Ile															•	1680
	acc Thr		Lys	Ile	Tyr	Asn	Pro	His	Gly	Gln	Asn		Val		Val		1728
	cac His																1776
	cac His																1824
gcg Ala	ggt Gly 610	acc Thr	tcc Ser	tac Tyr	gcc Ala	acc Thr 615	cac His	ggc Gly	aag Lys	gcc Ala	atg Met 620	att Ile	ccg Pro	ctg Leu	tac Tyr		1872
atc	ttc	tac	tcg	atg	ttc	gga	ttc	cag	cgc	acc	ggt	gac	tcc	atc	tgg		1920

Ile 625	Phe	Tyr	Ser	Met	Phe 630	Gly	Phe	Gln	Arg	Thr 635	Gly	Asp	Ser	Ile	Trp 640	
					atg Met											1968
		Thr			acc Thr											2016
					tcc Ser											2064
					atc Ile											2112
					aag Lys 710											2160
					cca Pro											2208
					ggc Gly											2256
					atc Ile											2304
	Lys	Āla	Ala	Ser	atc Ile	Leu	Glu	Ala	Asp	Tyr	Gly	Val				2352
					tct Ser 790											2400
_		_		_	ctg Leu	_				_	_	_			_	2448
					ctg Leu											2496
tct	gac	ttc	tcc	act	gat	ctg	сса	aac	cag	atc	cgt	gaa	tgg	gtc	сса	2544

Ser	Asp	Phe 835	Ser	Thr	Asp	Leu	Pro 840	Asn	Gln	Ile	Arg	Glu 845	Trp	Val	Pro		
												ttc Phe				2592	
cgc Arg 865	cca Pro	gct Ala	gct Ala	cgt Arg	cgc Arg 870	ttc Phe	ttc Phe	aac Asn	atc Ile	gac Asp 875	gct Ala	gag Glu	tcc Ser	att Ile	gtt Val 880	2640	
												atc Ile				2688	
												gat Asp				2736	
					aac Asn						•					2766	
															•		
<210)> 3	32													•		
<211		922								•							
<212		PRT			,	٠	-		70.00	20120	0.00						
<213	3> 1	3rev	Lbact	ceri	ım la	actoi	erme	entur	n ATC	CTS	369						
<400)> :	32				•											
Met 1	Ala	Asp	Gln	Ala 5	Lys	Leu	Gly	Gly	Lys 10	Pro	Ser	Asp	Asp	Ser 15	Asn	•	
Phe	Ala	Met	Tle 20	Arg	Asp	Gly	Val	Ala 25	Ser	Tyr	Leu	Asn	Asp 30	Ser	Asp		
Pro	Glu	Glu 35	Thr	Asn	Glu	Trp	Met 40	Asp	Ser	Leu	Asp	Gly 45	Leu	Leu	Gln		
Glu	Ser 50	Ser	Pro	Glu	Arg	Ala 55	Arg	Tyr	Leu	Met	Leu 60	Arg	Leu	Leu	Glu		
Arg	717	Ser	Ala	Lvs	Arg	Val	Ser	Leu	Pro		Met	Thr	Ser	Thr	Asp 80		
65	ніа	DCI	,	3	70					75					00	*	
				,	70	Thr	Ser	Met	Glų		Glu	Phe	Pro	Gly		•	
				,	70	Thr	Ser	Met		Pro	Glu	Phe	Pro	Gly			
				,	70	Thr	Ser	Met	Glu -14	Pro	Glu	Phe	Pro	Gly			
				,	70	Thr	Ser	Met		Pro	Glu	Phe	Pro	Gly			

Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala Ile Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly His Ile Ser Thr Tyr Ala Gly Ala Ala Pro Leu Tyr Glu Val Gly Phe Asn His Phe Phe Arg Gly Lys Asp His Pro Gly Gly Gly Asp Gln Ile Phe 150. Phe Gln Gly His Ala Ser Pro Gly Met Tyr Ala Arg Ala Phe Met Glu Gly Arg Leu Ser Glu Asp Asp Leu Asp Gly Phe Arg Gln Glu Val Ser Arg Glu Gln Gly Gly Ile Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr Phe Val Val Asn Cys Asn Leu Gln Arg Leu 280 -

Asp Gly Pro Val Arq Gly Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser

290 295 300

Phe 305	Phe	Arg	Gly	Ala	G1y 310	Trp	Ser	Val	Ile	Lys 315	Val	Val	Trp	GIY	Arg 320
Glu	Trp	Asp	Glu	Leu 325	Leu	Glu	Lys	Asp	Gln 330	Asp	Gly	Ala	Leu	Val 335	Glu
Ile	.Met	Asn	Asn 340	Thr	Ser	Asp	Gly	Asp 345	Tyr	Gln	Thr	Phe	Lys 350	Ala	Asn
Asp	Gly	Ala 355	Tyr	Val	Arg	Glu	His 360	Phe	Phe	Gly	Arg	Asp 365	Pro	Arg	Thr
Ala	Lys 370	Leu	Val [.]	Glu	Asn	Met 375	Thr	Asp.	Glu	Glu	Ile 380	Trp	Lys	Leu	Pro
Arg 385	Gly	Gly	His	Asp	Tyr 390	Arg	Lys	Val	Tyr	Ala 395	Ala	Tyr	Lys	Arg	Ala 400
Leu	Glu	Thr	Lys	Asp 405	Arg	Pro	Thr	Val	Ile 410	Leu	Ala	His	Thr	Ile 415	Ļys
Gly	Tyr	Gly	Leu 420	Gly	His	Asn	Phe	Glu 425	Gly	Arg	Asn	Ala	Thr 430	His	Gln
Met	Lys	Lys 435	Leu	Thr	Leu	Asp	Asp 440	Leu	Lys	Leu	Phe	Arg 445	Asp	Lys	Gln
Gly	Ile 450	Pro	Ile	Thr	Asp	Glu 455	Gln	Leu	Glu	Lys	Asp 460	Pro	Tyr	Leu	Pro
Pro 465	Tyr	Tyr	His	Pro	Gly 470	Glu	Asp	Ala	Pro	Glu 475	Ile	Lys	Tyr	Met	Lys 480
Glu	Arg	Arg	Ala	Ala 485	Leu	Gly	Gly	Tyr	Leu 490	Pro	Glu	Arg	Arg	Glu 495	Asn
Tvr	Asp	Pro	Tle	Gln	Val	Pro	Pro	Leu	Asp	Lvs	Leu	Ara	Ser	Val	Ara

Lys Gly Ser Gly Lys Gln Gln Ile Ala Thr Thr Met Ala Thr Val Arg 515 520 525

Thr Phe Lys Glu Leu Met Arg Asp Lys Gly Leu Ala Asp Arg Leu Val 530 540

Pro Ile Ile Pro Asp Glu Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe 545 550 555 560

Pro Thr Leu Lys Ile Tyr Asn Pro His Gly Gln Asn Tyr Val Pro Val 565 570 575

Asp His Asp Leu Met Leu Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile 580 585 590

Leu His Glu Gly Ile Asn Glu Ala Gly Ser Val Ala Ser Phe Ile Ala 595 600 605

Ala Gly Thr Ser Tyr Ala Thr His Gly Lys Ala Met Ile Pro Leu Tyr 610 615 620

Ile Phe Tyr Ser Met Phe Gly Phe Gln Arg Thr Gly Asp Ser Ile Trp
625 630 635

Ala Ala Asp Gln Met Ala Arg Gly Phe Leu Leu Gly Ala Thr Ala 645 650 655

Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln His Met Asp Gly His 660 665 670

Ser Pro Val Leu Ala Ser Thr Asn Glu Gly Val Glu Thr Tyr Asp Pro 675 680 685

Ser Phe Ala Tyr Glu Ile Ala His Leu Val His Arg Gly Ile Asp Arg 690 695 700

Met Tyr Gly Pro Gly Lys Gly Glu Asp Val Ile Tyr Tyr Ile Thr Ile

Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu Pro Glu Gly Leu Asp Val 725 730 735

Glu Gly Leu His Lys Gly Ile Tyr Leu Tyr Ser Arg Gly Glu Gly Thr 740 745 750

Gly His Glu Ala Asn Ile Leu Ala Ser Gly Val Gly Met Gln Trp Ala 765

Leu Lys Ala Ala Ser Ile Leu Glu Ala Asp Tyr Gly Val Arg Ala Asn 770 780

Ile Tyr Ser Ala Thr Ser Trp Val Asn Leu Ala Arg Asp Gly Ala Ala 785 790 795

Arg Asn Lys Ala Gln Leu Arg Asn Pro Gly Ala Asp Ala Gly Glu Ala 805 810

Phe Val Thr Gln Leu Lys Gln Thr Ser Gly Pro Tyr Val Ala Val 820 825

Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu Trp Val Pro 835

Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr 850 855

Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu Ser Ile Val 865 870 875

Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile Asp Val Ser 895

Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp Pro Thr Ser 900 905 910

Val Ser Val Asp Pro Asn Ala Pro Glu Glu

```
33
<210>
<211>
       8556
       DNA
      Brevibacterium lactofermentum ATCC13869
<213>
<220>
       CDS
<221>
       (2360)..(5125)
<222>
<223>
<400>
       33
tcacgttacg gcgatcaaca ccgcaaccac tacgagaaga tctccaaacg agaccaagag
                                                                    60
cgcttctaag cccgtctcat tttgcacctg ccattctgtg aggatatggc aggtgctttt
                                                                   120
tcatgccact atcttggggt tctcggtatt agatcttctg ataaaaaccc gatagttttc
                                                                   180
                                                                   240
ttgcgctaga cactaattac ggcaccgctt aagcatggtc gtgacacgta aaacctgact
taggccattt tgatgtggtg tagatcatat tgacgtcaat gaatgaagtg actaactccg
                                                                    300
ccgaatccac atcgtctaaa aggcctgggc gaccacgtaa agacgggcac gacgagaaga
                                                                    360
tcatcgacgc aactttacgg ctcatcgaca gcaatcgtcc cgtcacggtc aatgcagttg
                                                                    420
 tcaaagaaag cggagtggca cgtgcagcgg tttatcgacg ctggcccagg ctagtggatc
                                                                    480
 tagtagcgga agctttagat gccgggcgag ctccagttga aatagatacc ccaggggaca
                                                                    540
 tcaaagagac cttgattgat gggctgttta caaatcaggc gaaaaccact ggagtctcct
                                                                    600
 atcctcgtca gcgatttcgc aaacggctcg agttggtgat gtcagatcaa gaattacagc
                                                                    660
 togoctaatg gaattoacat gtgaagagac gtcgagaago aaatattogo gogotgcaag
                                                                    720
                                                                    780
 tegegeaaga aaaaggeeaa ateegggegg atetagaeat egaggegtge etegatgeaa
 tccttggggt gttttattac caatcggtcg cgcgtggagt aaatttcacc gaccaaggta
                                                                     840
 900
                                                                     960
 aggttctgac gaggtgcgaa gcaagttgtc gcgcgccgca cctcagtatc cggatcaact
 taatttcgaa gtgctgggtt ttctcgcgca tacccaatgc gtaccgatgt gcccatgagc
                                                                    1020
 gaaaaacagg ccacgataag tttcttaaaa cttatcgtgg cctgcttcta tatttgtgcg
                                                                    1080
  ccctgacggg ctcgaaccgc cgacctgctg ggtgtaaacc agctgctctt ccagctgagc
                                                                    1140
```

taaaggcgcg cacgtgc	tt tctagaacca	ccttggtggc	ctcgaaagca	acgagtgaaa	1200
tactaacaca caatctco	cac agacctaaaa	tcgctgctca	ggccgtggaa	attagcgatt	1260
gttaaggctt cttgtttc	cca cgctggacga	ggcaagaacc	ttgccaatta	ccgagacgtt	1320
ccgccttggt ctgcacga	aga cctgccagtt	gtgctgattc	agagataact	ccaggagcca	1380
gggctccttc tttaccaa	atg ccaggagtca	acacccagat	acgaccattc	tcagcgaggg	1440
agcggatgga atccaca	agt ccgtcgacga	gatcgccgtc	atcctcgcgc	caccagagca	1500
gcacgacatc gcacage	cg tcggtttctt	catcgagtag	ttcctcaccg	attgcatctt	1560
cgatggactc gctgatca	agc gtgtcggaat	cttcatccca	tccaatttct	tgaacgatat	1620
gacccgattg aatgccga	agt agttgagcat	aatcctgggc	accttgcttg	actgcgcccg	1680
gagcgtcggc cacttta	ata atcctcctcg	tgtgggcccc	gatgtgtttt	tcgattacat	1740
ggattcaaca tgaaacc	gcg gggctattga	tatatccgaa	ttgcacatta	ccgtccaacc	1800
ggtactttga accacct	tc cctggaattt	tttccttttc	ctccccttt	acgctcaaga	1860
atcaatgaat tcaatca	ctg gccagcgatt	aacttttcga	gttttcagtc	ttggatttcc	1920
acaattctct tcaaaata	aat ggtggctaga	tttttcatca	aaccctcacc	aaaaggacat	1980
cagacctgta gttttate	gcg attcgcgtca	aacgtgagag	aaacatcaca	tctcacggga	2040
aactacccga taattct	tg caaaactttg	caaagggtaa	tgaacatgca	gctagtttcc	2100
gtagaaatgt tctttaa	aaa atccacaaca	attgccagga	agcacaccga	ttgatggata	2160
cctgaaatcc cagtgag	ege accactecco	ttacgtcaca	gtctgtaaaa	caaatcttcg	2220
gtgttgcgta tccttgt	taa taacttatgo	gttgacccat	tcgtgcactt	cggtgtgcca	2280
caattaggta cgaccaa	gaa tgggaccggg	aaaccgggac	gtataaacga	aataaaacat	2340
tccaacagga ggtgtgg		. caa gca aaa 9 Gln Ala Ly: .5			2392
tcg gat gac tct aad Ser Asp Asp Ser Ass 15					2440
ttg aac gac tca ga Leu Asn Asp Ser As 30	t ccg gag gag p Pro Glu Glu 35	acc aac gag Thr Asn Glu	tgg atg ga Trp Met As 40	t tca ctc p Ser Leu	2488

				cca Pro				2536
				gca Ala				2584
				acc				2632
				gag Glu 100				2680
				cac His				2728
				tac Tyr				2776
				cgc Arg				2824
				cac His				2872
				tct Ser 180				2920
				ggt Gly				2968
				gag Glu				3016
				cag. Gln				3064
				tct Ser				-3112

											cgt Arg					310	60
											ttc Phe					320	80
											aac Asn 295					325	56
											tgg Trp					33(04
gtt Val	gtt Val	tgg Trp	ggt Gly	cgc Arg 320	gag Glu	tgg Trp	gat Asp	gaa Glu	ctt Leu 325	ctg Leu	gag Glu	aag Lys	gac Asp	cag Gln 330	gat 'Asp	335	52
											gat Asp					340	00
								Tyr			gag Glu					344	48
											atg Met 375					34	96
atc Ile 380	tgg Trp	aag Lys	ctg Leu	cca Pro	cgt Arg 385	ggc Gl _. y	ggc Gly	cac His	gat Asp	tac Tyr 390	cgc Arg	aag Lys	gtt Val	tac Tyr	gca Ala 395	35	44
gcc Ala	tac Tyr	aag Lys	cga Arg	gct Ala 400	ctt Leu	gag Glu	acc Thr	aag Lys	gat Asp 405	cgc Arg	cca Pro	acc Thr	gtc Val	atc Ile 410	ctt Leu	. 35	92
gct Ala	cac His	acc Thr	att Ile 415	aag Lys	ggc Gly	tac Tyr	gga Gly	ctc Leu 420	ggc Gly	cac His	aac Asn	ttc Phe	gaa Glu 425	ggc Gly	cgt Arg	36	40
											gat Asp					36	88
											gag Glu 455					37	36

gat Asp 460	cct Pro	tac Tyr	ctt Leu	cct Pro	cct Pro ' 465	tac Tyr	tac (Tyr 1	cac His	cca Pro	ggt Gly 470	gaa Glu	gac Asp	gct Ala	cct Pro	gaa Glu 475	37	784
atc Ile	aag Lys	tac Tyr	atg Met	aag Lys 480	gaa Glu	cgt Arg	cgc Arg	gca Ala	gcg Ala 485	ctc Leu	ggt Gly	ggc	tac Tyr	ctg Leu 490	cca Pro	38	332
gag Glu	cgt Arg	cgt Arg	gag Glu 495	aac Asn	tac Tyr	gat Asp	cca Pro	att Ile 500	cag Gln	gtt Val	cca Pro	cca Pro	ctg Leu 505	gat Asp	aag Lys	. 3	380
ctt Leu	cgc Arg	tct Ser 510	gtc Val	cgt Arg	aag Lys	ggc Gly	tcc Ser 515	ggc Gly	aag Lys	cag Gln	cag Gln	atc Ile 520	gct Ala	acc Thr	act Thr	3	928
atg Met	gcg Ala 525	act Thr	gtt Val	cgt Arg	acc Thr	ttc Phe 530	aag Lys	gaa Glu	ctg ¡Leu	atg. Met	cgc Arg 535		aag Lys	ggc Gly	ttg Leu		976
gct Ala 540	gat Asp	cgc Arg	ctt Leu	gtc Val	cca Pro 545	atc Ile	att Ile	cct Pro	gat Asp	gag Glu 550	2320	ı cgt ı Arg	acc	ttc Phe	ggt Gly 555	4	024
		tct Ser	tgo Trp	ttc Phe 560	Pro	acc Thr	ttg Leu	aag Lys	atc Ile 565	. <u>- y</u> -	aac Asr	c ccg	cac His	ggt Gly 570	cag Gln		1072
aac Asr	tac Tyr	gtç Val	g cct L Pro 575	o Val	gac Asp	cac His	gac Asp	ctg Leu 580	rict	g cto Lev	tco Sei	c tac r Tyı	c cgt Arg 585	-	g gca 1 Ala	:- "	4120
cct Pro	gaa Glu	a gga a Gly 590	a cad		c ctg e Leu	cac His	gaa Glu 595	ו פד7	ato Ile	c aad e Asr	gae n Gl	g gct u Ala 600		t tco y Sei	c gtg r Val	•	4168
gc	a tog a Sei 60!	g tto		c gct e Ala	gcg a Ala	g ggt a Gly 610	1111	tco Ser	c tac	c gco r Ala	c ac a Th 61	_	c gg s Gl	c aa y Ly	g gcc s Ala		4216
at Me 62	g at		g ct o Le	g ta u Ty	c ato r Ile 625	e Pne	c tac e Ty:	tc Se	g at r Me	g tt t Ph 63	0 0 -	a tt y Ph	c ca e Gl	g cg n Ar	c acc g Thr 635		4264
·		c tc p Se	c at	c tg e Tr 64	b AT	a gc	a gco a Ala	c ga a As	t ca p Gl 64		g gc t Al	ca cg La Ar	t gg g Gl	c tt y Ph 65	c cto le Leu 50	1	4312
tt Le	g gg u Gl	c gc y Al	t ac a Th	ır Al	a gg a Gl	t cg y Ar	c ac g Th	c ac r Th 66	т пс	g ac eu Th	c gg ir Gl	gt ga Ly Gl	a go Lu Gl	jc ct .y L∈ 55	c caq eu Glr	g n	4360
													•				•
									-	23-							

					tcc Ser											4408	
					tcc Ser											4456	
					atg Met 705											4504	
					tac Tyr											4552	
gaa Glu	gga Gly	ctg Leu	gac Asp 735	gta Val	gaa Glu	ggc Gly	ctg Leu	cac His 740	aag Lys	ggc Gly	atc Ile	tac Tyr	ctc Leu 745	tac Tyr	tcc Ser	4600	
					ggc Gly											4648	
					ctc Leu											4696	
					att Ile 785											4744	
cgc Arg	gat Asp	ggc Gly	gct Ala	gct Ala 800	cgt Arg	aac Asn	aag Lys	gca Ala	cag Gln 805	ctg Leu	cgc Arg	aac Asn	cca Pro	ggt Gly 810	gca Ala	4792	
					ttc Phe											4840	*
					tct Ser											4888	•
					ggc Gly											4936	
					cgc Arg 865											4984	
									-24-	-							

gct gag tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa ggc Ala Glu Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly 880 885	5032
aag atc gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag ttg Lys Ile Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu 895	5080
gat gat cct acg agt gtt tcc gta gat cca aac gct cct gag gaa Asp Asp Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu 910 915	5125
taaatcacct caagggacag ataaatcccg ccgccagacg ttagtctggc ggcgggattc	5185
gtcgtaaagc aagctctttt tagccgagaa acgccttgtc agacaatgtt gcgcccttga	5245
tattggcgaa ctcctgcagc aaatcgcgca cagtcaactt cgacttggta gcctgatctg	5305
cctggtagac aatctggcct tcatgcatca tgatcaggcg attgcccagg cgaattgcct	5365
gttccatgtt gtgcgtgacc ataagcgtag tcagagttcc atctgccacg atctttcgg	5425
gttccatgtt gtgcgtgacc ataaycgtag coagagas tgcggtgtgc tcatccaaca	5485
tcaaggtggt cacaagctct gcacgctgtg gatcaagcgc tgcggtgtgc tcatccaaca	5545
gcatgatttt aggttgagta aaaccagcca tcagcaggga caatgcctga cgctgaccgc	5605
cagagagcaa accaactttg gcagtgagcc tgttttccag acccagctca aggcgctcaa	
gttcctgctt gaattgctca cggcgcttcg aggtcagtgc aaagcccaat ccacggcgct	5665
tgccgcgcag caacgcgatg gccagattct cttcaatggt gagattcggc gcggtgcctg	5725
ccaaaggatc ctgaaaaacg cggccgatgt agcgggcacg cttgtgctct gacatcttgt	5785
ttaccttgtt gccgtcgatg gaaatctcgc cggaatcaac aagcaaacgg ccagaaacag	5845
cgttgagcag ggtggattta cccgcaccgt tagaaccgat gacggtgaca aaatcgccct	5905
cagccatate gagtttgage tgctgcaacg egeggegete atteacagtg eeggggaaga	5965
aggttttgga aattccgttg atggataaca tgtcttaagc ctccactgct actggttgct	6025
taggettegg tgeettggag aacttegeae gecaeetegg eageageatg gegaeaacea	6085
ccaagatcgc agaaattgcc ttcatatcgt tggggtcaag gccaacgcgc agtgctgcga	6145
aaatgatcag gcggtacgcg atggcaccga cgatgacagc caacacagcc aaccacacgc	6205
gacgetgace gaagatggee tggeeceaaa ataacegatg egagacegat caegatgagg	6265
gacgetgace gaagatggee tygeeceaaa deddoogaay y y y ceaataceca tegaaatate tgegaageee tggtactgag egatgagtge aceggeaaga	6325
ccaataccca togaaatato tgogaagooo tggoudtg-9 -5 5 5 5	

6385 ccaacagaac cattggacag ggagatggtg aggattttgg tgaaatccgt tgaaacacca 6445 aaggactgca ccatcggccc gttgtcgccg gtggatcgca gcgacagtcc gatatcagtg 6505 ttgaggaacc agatgacgat gagtcccaaa aatcccactg caacggcgag gatcgccggg cctgcccatg tgccgaggag gccggcgtcg cgaagcgggg tgaagaggtt atcggtgcgc 6565 6625 aacaatggca cgttcgcgcc acccatgatg cgcaagttaa ccgaccacaa cgcaatcatg 6685 gtcaaaatac ctgcgagcaa accatcgatc ttgcccttgg tgtgcagcaa accggtgatc 6745 atgccagcga taaagccagt aacgaaacca gcggcagtag ccataagagg aggccagcca 6805 gacataagag ctgtcgcagc tgttgccgcg ccagtggtca ggctgccgtc aacggtgagg 6865 tcgggaaagt tgagcacacg gaacgtcaaa tagacgccca atgcgacaac tccgtacaac 6925 aatccgaact caaaagcgcc gatcatacgc gttcggcctt atccaaaatc tcttgaggga 6985 tetecaegee etggegetet getgeatett egttgateae gtaggtgaae teagttgeag tctccacagg catggttgct gggtcttcgc cgtcctgcag aatacgcaga gccatctcgc 7045 7105 cagtctggcg gccaagctcg gtgtaatcga tacccagggt tgccagtgcg ccaccctcaa 7165 cagtgccgga ctcagcaccg atcacaggga tctgcttctg ctcagcaacc tgaaccagag 7225 aagaaatacc ggaaacaacc atgttgtcag ttggaacgta gatgacatca acatcgccga 7285 gagetteaac ageetgetga atetegttea eggtagtgae agtetgagta ttaaeggaea 7345 gccccagtgg ctcagcagcc ttggtgacct catcgacctg cacctgagag ttgacctcac 7405 cagacgcgta gacgatgccg atggactttg cgtcaggaac cagctgctgc aaaagctcca actgctgctc aatcggtgcg atatcagaag taccggtgac gtttccgcca ggtgcttcat 7465 7525 tagaatccac cagctctgcc gacactgcat cggtaactgc ggtgaacagg actgggatat 7585 cagtgatatt ctgcgcagtt gcctgtgctg ctggagttgc aacagccaac acgagatcca 7645 . aattgtcaga agcgaactgc tgagaaatag tcagtgcagt gccctgctcg ccgttagcgt 7705 tttgctcatc aaaggtgacg tcaacgcctg cctcttcaaa agcttccttg aaaccagtgg 7765 tcgctgcatc aagtgcaggg tgctgaacaa gctggttgat gccaactcgg taagagtcgc 7825 cacctgcage atcagtggag gtggagetgt cactggaate gettgageae gaagecaaeg 7885 ccaaggcgcc aacagtaaag atgcttgcga gtaccttcga acgggaagaa aacatagcac

atctccttaa agtgttattt tcaaaaaggg gcagacagcg tcaacacatg tctcggataa 7945 8005 agaaccatat gtgaaatgtc tcatgattta aactacttgt tctaccagtc atatgcgcaa 8065 ttccccctqq atatcccqca qqacatqqac aaaatqqqtg gataqcqqqt gcaccaattc aatcttttaa aggccctaga caccgcgatt tccttaatcg atcattaaag agggatcctc 8125 tcccctaaca aacctccaaa gactagagtg gggaacacca tgaacgtttc ctcaaataaa 8185 cccaqtqact ctqaccqcqa atatcttcaa tcagaactca cccggctcgt tggccagggg 8245 cgactcgatc tagatactta.ccaagacgtg gttgataccg tttggtctac tgatgatcta 8305 qqcqaqttqa tqaqqatccq tqcccqcttc ctgggagggc cgcaggtttc gcagcagcgg 8365 8425 ccccaqcaqc cqcaqcaacc acatcagcgg ccgcaacagc aaccgccaca gcattatgga caaccegget acggecaate aceteaatat ceacegeage ageeteegea taateageee 8485 ggctattacc ccqatcccqq ccctqqccaq caqcaaccac cqatqcacca gccaccaacq 8545 8556 cqtccaaatc a

<210> 34

<211> 922

<212> PRT

<213> Brevibacterium lactofermentum ATCC13869

<400> 34

Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp 20 25 30

Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln 35 40 45

Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu 50 55 60

Arg Ala Ser Ala Lys Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp 65 70 75 80

Tyr	Val	Asn	Thr	Ile 85	Pro	Thr	Ser	Met	Glu 90	Pro	Glu	Phe	Pro	Gly 95	Asp
Glu	Glu	Met	Glu 100	Lys	Arg	Tyr	Arg	Arg 105	Trp	Ile	Arg	Trp	Asn 110	Ala	Ala
Ile	Met	Val 115	His	Arg	Ala	Gln	Arg 120	Pro	Gly	Ile	Gly	Val 125	Gly	Gly	His
Ile	Ser 130	Thr	Tyr	Ala	Gly	Ala 135	Ala	Pro	Leu	Tyr	Glu 140	Val	Gly	Phe	Asn
His 145	Phe	Phe	Arg	Gly	Lys 150	Asp	His	Pro	Gly	Gly 155	Gly	Asp	Gln	Ile	Phe 160
Phe	Gln	Glý	His	Ala 165	Ser	Pro	Gly	Met	Tyr 170	Ala	Arg	Ala	Phe	Met 175	Glu
Gly	Arg	Leu	Ser 180	Glu	Asp	Asp	Leu	Asp 185	Gly	Phe	Arg	Gln	Glu 190	Val	Ser
Arg	Glu	Gln 195	Gly	Gly	Ile	Pro	Ser 200	Tyr	Pro	His	Pro	His 205	Gly	Met	Lys
Asp	Phe 210	Trp	Glu	Phe	Pro	Thr 215	Val	Ser	Met	Gly	Leu 220	Gly	Pro	Met	Asp
Ala 225	Ile	Tyr	Gln	Ala	Arg 230	Phe	Asn	Arg	Tyr	Leu 235	Glu	Asn	Arg	Gly	Ile 240
Lys	Asp	Thr	Ser	Asp 245	Gln	His	Val	Trp	Ala 250	Phe	Leu	Gly	Asp	Gly 255	Glu
Met	Asp	Glu	Pro 260	Glu	Ser	Arg	Gly	Leu 265	Ile	Gln	Gln	Ala	Äla 270	Leu	Asr
Asn	Leu	Asp 275	Asn	Leu	Thr	Phe	Val 280	Val	Asn	Cys	Asn	Leu 285	Gln	Arg	Leu

Asp	Gly 290	Pro	Val	Arg	Gly	Asn 295	Thr	Lys	Ile	Ile	Gln 300	Glu	Leu	Glu	Ser
Phe 305	Phe	Arg	Gly	Ala	Gly 310	Trp	Ser	Val	Ile	Lys 315	Val	Val	Trp	Gly	Arg 320
Glu	Trp	Asp	Glu	Leu 325	Leu	Glu	Lys	Asp	Gln 330	Asp	Gly	Ala	Leu	Val 335	Glu
Ile	Met	Asn	Asn 340	Thr		Asp	Gly	Asp 345	Tyr	Gln	Thr	Phe	Lys 350	Ala	Asn
Asp	Gly	Ala 355		Val	Arg	Glu	His 360	Phe	Phe	Gly	Arg	Asp 365	Pro	Arg	Thr
Ala	Lys 370		Val	Glu	Asn	Met 375	Thr	Asp	Glu	Glu	Ile 380	Trp	Lys	Leu	Pro
Arc	Gly	Gly	His	Asp	Tyr 390	Arg	Lys	Val	Tyr	Ala 395	Ala	Tyr	Lys	Arg	Ala 400
Leı	ı Glu	ı Thr	Lys	Asp 405	Arg	Pro	Thr	Val	. Il∈ 410	e Leu	ı Ala	. His	Thr	11e 415	Lys
Gl	у Туг	c Gly	y Let 420	ı Gly	/ His	s Asr	n Phe	e Glu 425	ı Gly	, Arc	g Asr	n Alá	a Thr 430	His	s Glr
Me	t Lys	s Lys 43	s Lei	u Thi	r Leı	ı Asp	Asp Asp 440	o Lei	ı Lys	s Lei	ı Phe	44	g Asp	o Lys	s Glr
Gl	y Ile 45		o Il	e Th	r Asj	o Gl	u Gli 5	n Lei	a Gli	u Ly	s Ası 460	o Pro	о, Ту:	r Le	ı Pr

470 480

Pro Tyr Tyr His Pro Gly Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys

Glu Arg Arg Ala Ala Leu Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn

485

Tyr	Asp	Pro	Ile 500	Gln	Val	Pro	Pro	Leu 505	Asp	Lys	Leu	Arg	Ser 510	Val	Arg
Lys	Gly	Ser 515	Gly	Lys	Gln	Gln	Ile 520	Ala	Thr	Thr	Met	Ala 525	Thr	Val	Arg
Thr	Phe 530	Lys	Glu	Leu	Met	Arg 535	Asp	Lys	Gly	Leu	Ala 540	Asp	Arg	Leu	Val
Pro 545	Ile	Ile	Pro	Asp	Glu 550	Ala	Arg	Thr	Phe	Gly 555	Leu	Asp	Ser	Trp	Phe 560
Pro	Thr	Leu	Lys	Ile 565	Tyr	Asn	Pro	His	Gly 570	Gln	Asn	Tyr	Val	Pro 575	Val
Asp	His	Asp	Leu 580	Met	Leu	Ser	Tyr	Arg 585	Glu	Ala	Pro	Glu	Gly 590	Gln	Ile
Leu	His	Glu 595		Ile	Asn	Glu	Ala 600	Gly	Ser	Val	Ala	Ser 605	Phe	Ile	Ala
Ala	Gly 610		Ser	Tyr	Ala	Thr 615	His	Gly	Lys	Ala	Met 620	Ile	Pro	Leu	Туг
Ile 625		e Tyr	Ser	Met	Phe 630	: Gly	Phe	Gln	Arg	Thr 635	Gly	Asp	Ser	Ile	Trp 640
Ala	a Ala	a Ala	a Asp	Glr 645	n Met	Ala	a Arg	ι Gly	Phe 650	e Leu	ı Leu	Gly	, Ala	Thr 655	Ala
Gly	y Arq	g Thi	Th:	r Lei	ı Thi	c Gly	/ Glu	Gly 665	Leu i	ı Glr	n His	s Met	Asp 670	o Gly	His
Sei	r Pro	o Vai		u Ala	a Sei	r Thi	c Asr 680	n Glu)	ı Gly	y Vai	l Glu	Th:	r Tyi	. Asp	Pro
Se	r Ph 69		а Ту	r Gl	u Il	e Ala 69	a His 5	s Lei	ı Val	l Hi:	s Aro	g Gl	y Il	e Asp	a Arg

Met 705	Tyr	Gly	Pro	Gly	Lys 710	Gly	Glu	Asp	Val	Ile 715	Tyr	Tyr	Ile	Thr	Ile 720
Tyr	Asn	Glu	Pro	Thr [.] 725	Pro	Gln	Pro	Ala	Glu 730	Pro	Glu	Gly	Leu	Asp 735	Val
Glu	Gly	Leu	His 740	Lys	Gly	Ile	Tyr	Leu 745	Tyr	Ser	Arg	Gly	Glu 750	Gly	Thr
Gly	His	Glu 755	Ala	Asn	Ile	Leu	Ala 760	Ser	Gly	Val	Gly	Met 765	Gln	Trp	Ala
Leu	Lys 770	Ala	Ala	Ser	Ile	Leu 775	Glu	Ala	Asp	Tyr	Gly 780	Val	Arg	Ala	Asn
Ile 785	Tyr	Ser	Ala	Thr	Ser 790	Trp	Val	Asn		Ala 795	Arg	Asp	Gly	Ala	Ala 800
Arg	Asn	Lys	Ala	Gln 805	Leu	Arg	Asn	Pro	Gly 810	Ala	Asp	Ala	Gly	Glu 815	Ala
Phe	Val	Thr	Thr 820	Gln	Leu	Lys	Gln	Thr 825	Ser	Gly	Pro	Tyr	Val 830	Ala	Val
Ser		Phe .835	Ser	Thr	Asp	Leu	Pro 840	Asn	Gln	Ile	Arg	Glu 845	Trp	Val	Pro
Gly	Asp 850	Tyr	Thr	Val	Leu	Gly 855	Ala	Asp	Gly	Phe	Gly 860	Phe	Ser	Asp	Thr
Arg 865	Pro	Ala	Ala	Arg	Arg 870	Phe	Phe	Asn	Ile	Asp 875	Ala	Glu	Ser	Ile	Val 880
Val	Ala	Val	Leu	Asn 885	Ser	Leu	Ala	Arg	Glu 890	Gly	Lys	Ile	Asp	Val 895	Ser
Val	Ala	Ala	Gln	Ala	Ala	Glu	Lys	Phe		Leu	Asp	Asp	Pro		Ser

Val Se	r Val Asp Pro Asn Ala Pro Glu Glu 915 920	
<210> <211> <212> <213>	35 20 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400> aatgcca	35 agga gtcaacaccc	.20
<210> <211> <212> <213>	36 20 DNA Artificial sequence	
<220> <223>	Synthetic DNA ,	
<400> acatgga	36 aaca ggcaattcgc	20
<210> · <211> <212> <213>	37 28 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400> cgtccc	37 gggc tgtaaaacaa atcttcgg	28
<210> <211> <212> <213>	38 27 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400> atcccc	38 gggc ttaccaccaa gttttgc	27

<210> <211> <212> <213>	39 30 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400> cttatg	39 cgtt gccacattcg tgcacttcgg	30
<210> <211> <212> <213>	40 40 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400> gcgttg	40 accc attcgtgcac ttcggtgtgc tataattagg	40
<210><211><211><212><213>	41 40 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400> gcgttg	41 ccac attcgtgcac ttcggtgtgc tataattagg	40
<210> <211> <212> <213>	42 38 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400> ttttaa	42 aacg ttctggagaa gactcctgga gtaatccg	38
<210><211><211><212><213>	43 20 DNA Artificial sequence	

<220> <223>	Synthetic DNA	
<400> cgatct	43 tgcc ttcgcgtgcc	20
<210> <211> <212> <213>	44 30 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400> agaccg	44 ccgg agtatgcaag aacgatgcgg	30
<210> <211> <212> <213>	45 30 DNA Artificial sequence	•
<220> <223>	Synthetic DNA	
<400> gacttc	45 acca tcaatcatct tcttcaggta	30
<210> <211> <212> <213>	46 30 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400> accttc	46 gacc agaccctggc taagggcttt	30 -
<210> <211> <212> <213>	47 30 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400>	47	

gctaaca	aagc gcgatcgcga	agctggcaac				30
<210> <211> <212> <213>	48 25 DNA Artificial sequ	ience			• • • • • • • • • • • • • • • • • • • •	
<220> <223>	Synthetic DNA	•	·			
<400> gcgatg	48 acac cgtttttgtt	ctcgc				2.5
<210><211><212><212><213>	49 25 DNA Artificial sequ	uence	· ·			
<220> <223>	Synthetic DNA	· · · · · · · · · · · · · · · · · · ·				
<400> ggcgac	49 atcc ttgcccagat	gatca	٠.			25
<210><211><212><213>	50 25 DNA Artificial seq	uence		·		*
<220> <223>	Synthetic DNA			,		
<400> gactto	50 cacca tcaatcatct	tette				25
<210> <211> <212> <213>	24 DNA	quence			10	٠.
<220> <223>			·			
<400> gccag	51 gtaca actgtctga	a ttgc				24
<210>	52					

<211> <212> <213>	DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400>	52 cgct tgccaatgca ggcaggtaag gtataacccg	40
gecaae		
<210><211><211><212>	53 40 DNA	
<213>	Artificial sequence	
<220> <223>	Synthetic DNA	,
<400> gttaat	53 cgct tgctaatgca ggcaggtaag gtataacccg	40
<210>	54	
<211> <212> <213>	40 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400>	54 cgct tgtcaatgca ggcaggtaag gtataacccg	40
geeda		
<210>	55	
<211>	40	
<212>	DNA	
<213>	Artificial sequence	
<220>		
<223>	Synthetic DNA	
<400>	55	
gttaat	togot tgttaatgca ggcaggtaag gtataatccg	40
<210>	56	
<211>	40	
<212>	DNA	
Z212N	Artificial sequence	

•

<223>	Synthetic DNA	
<400> gttaato	56 egct tgtcaatgca ggcaggtaag gtataatccg	40
<210> <211> <212> <213>	57 30 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400> gggttco	57 cagc ctcgtgcgga attcgtggag	30
<210> <211> <212> <213>	58 25 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400> gcgttac	58 ccca gagctggatc ctcgg	25
<210> <211> <212> <213>	59 16 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
	59 tggc tgatcg	16
<210> <211> <212> <213>	60 17 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400>	60	

ctttcc	caga ctctggc	1/
<210> <211> <212> <213>	61 21 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400> gctataa	61 attt gacgtgagca t	21
<210><211><211><212><213>	62 25 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400> gctcace	62 gtca aattatagca gtgtc	25
<210><211><211><212><213>	63 54 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400> ttgttg	63 tcat totgtgogac actgotàtaa tttgaacgtg agcagttaac agco	54
<210><211><211><212><213>	64 63 DNA Artificial sequence	
<220> <223>	Synthetic DNA	
<400> gttaac	64 tgct cacgttcaaa ttatagcagt gtcgcacaga atgacaacaa agaattaaaa	60
ttg		63

<210> <211>	65 25	
<211>	DNA	
<213>	Artificial sequence	
<220>		
<223>	Synthetic DNA	
<400>	65	
gctagc	ctcg ggagctctct aggag	25
<210>	66	
<211>	25	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic DNA	•
<400>	66	•
	ccc agactctggc cacgc	25